--154. A nucleic acid molecule, comprising a nucleotide sequence that comprises:

    a.   a transcription regulatory region;

    b.   a transcription termination moiety;

    c.   a linking moiety; and

    d.   an open reading frame.

155.   The nucleic acid molecule of claim 154, wherein said nucleic acid molecule comprises dsDNA or ssDNA.

156.   The nucleic acid molecule of claim 154, further comprising a ribosome binding sequence.

157.   The nucleic acid molecule of claim 154, wherein said transcription termination moiety is a DNA binding protein or a sequence having secondary structure.

158.   The nucleic acid molecule of claim 154, wherein said linking moiety is a tRNA mimetic, biotin, digoxigenin, nitrilotriacetic acid, a nucleic acid sequence, a peptide nucleic acid sequence, or a peptide sequence.

159.   The nucleic acid molecule of claim 154, wherein said linking moiety is puromycin.

160.   The nucleic acid molecule of claim 154, wherein said open reading frame comprises a random sequence or sequence of interest.

161.   The nucleic acid molecule of claim 154, further comprising a translational start codon.

162.   The nucleic acid of claim 154, further comprising a spacer region.

163.   The nucleic acid molecule of claim 160, wherein said nucleic acid molecule is operably linked to a polypeptide encoded by said random sequence or sequence of interest.

164.   The nucleic acid of claim 163 bound to a substance of interest.

165. The nucleic acid molecule of claim 164, wherein said substance of interest is on a solid support.

166. The nucleic acid molecule of claim 163, wherein said nucleic acid molecule is bound to a solid support.

167. A library of nucleic acid molecules of claim 160, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.

168. A library of nucleic acid molecules of claim 163, wherein said library is contacted with at least one substance of interest.

169. The library of nucleic acid molecules of claim 168, wherein said at least one substance of interest is directly or indirectly bound on a solid support or in solution.

170. The library of nucleic acid molecules of claim 167, wherein said library of nucleic acid molecules is on a solid support.

171.   A method for identifying a nucleic acid molecule, comprising:

    1.   providing a nucleic acid molecule of claim 160;

    2.   transcribing said nucleic acid molecule to provide a transcription complex, wherein said complex comprises a nucleic acid operably linked to a transcribed RNA;

    3.   translating said transcribed RNA to form a nucleic acid-polypeptide complex, wherein said nucleic acid-polypeptide complex comprises a nucleic acid operably linked to a polypeptide that the nucleic acid encodes;

    4.   contacting said nucleic acid-polypeptide complex with at least one substance of interest;

    5.   selecting at least one complex that binds with said at least one substance of interest; and

    6.   identifying said nucleic acid molecule.

172.   The method of claim 171, wherein said identifying comprises amplifying said random sequence or said nucleic acid sequence of interest.

173.   The method of claim 171, further comprising the step of sequencing the identified random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.

174.   The method of claim 171, further comprising performing steps 1, 2, 3, 4, and 5 reiteratively.

175. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest, comprising:

1) providing a nucleic acid molecule of claim 160;

2) transcribing said nucleic acid molecule to provide a transcription complex, wherein said complex comprises a nucleic acid operably linked to a transcribed RNA;

3) translating said transcribed RNA to form a nucleic acid-polypeptide complex, wherein said nucleic acid-polypeptide complex comprises a nucleic acid operably linked to a polypeptide that the nucleic acid encodes;

4) contacting said nucleic acid-polypeptide complex with at least one substance of interest;

5) selecting at least one complex that binds with said at least one substance of interest; and

6) identifying said nucleic acid molecule.

176. The method of claim 175, wherein said identifying comprises amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.

177. The method of claim 175, further comprising performing steps 1, 2, 3, 4, and 5 reiteratively.

178. A method for identifying a test compound, comprising:

    a)   contacting a target with a complex that comprises:

        1) a linking moiety;

        2) a nucleic acid molecule comprising an open reading frame; and

        3) a polypeptide encoded by said open reading frame;

        wherein said linking moiety is operably linked to said polypeptide;

    b)   identifying polypeptides bound with said target;

    c)   determining the structure of said polypeptide; and

    d)   identifying moieties that have structures that have space filling shapes that are similar to at least a portion of said polypeptide.

179. A method for identifying a target, comprising:

    a)   contacting a substance of interest with a complex that comprises:

        1)   a linking moiety;

        2)   a nucleic acid molecule comprising an open reading frame; and

        3)   a polypeptide encodied by said open reading frame;

        wherein said linking moiety is operably linked to said polypeptide; and

    b)   identifying targets that bind with said complex.

180. A nucleic acid molecule that comprises:

    a.   a linking moiety;

    b.   a random sequence or sequence of interest; and

    c.   a translational control sequence.

181. The nucleic acid molecule of claim 180, wherein said nucleic acid molecule comprises dsDNA, ssDNA, or ssRNA.

182. The nucleic acid molecule of claim 180, further comprising a ribosome stalling sequence.

183. The nucleic acid molecule of claim 180, further comprising at least one translational start codon.

184. The nucleic acid of claim 180, further comprising a spacer region.

185. The nucleic acid of claim 180, wherein said linking moiety is a tRNA mimetic, biotin, digoxigenin, nitrilotriacetic acid, a nucleic acid sequence, a peptide nucleic acid sequence, or a peptide sequence.

186. The nucleic acid of claim 180, wherein said linking moiety is puromycin.

187. The nucleic acid molecule of claim 180, wherein said nucleic acid molecule is operably linked to a polypeptide encoded by said random sequence or sequence of interest.

188. The nucleic acid molecule of claim 180, wherein said nucleic acid molecule is covalently linked to a polypeptide encoded by said random sequence or sequence of interest.

189. The nucleic acid of claim 187 bound to a substance of interest.

190. The nucleic acid molecule of claim 189, wherein said substance of interest is on a solid support.

191. The nucleic acid molecule of claim 188, wherein said nucleic acid molecule is bound to a solid support.

192.   A library of nucleic acid molecules of claim 180.

193.   A method for identifying a nucleic acid molecule or sequence, comprising:

1) providing at least one nucleic acid molecule of claim 181;

2) translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest;

3) contacting said at least one complex with at least one substance of interest;

4) selecting at least one complex that binds with said at least one substance of interest; and

5) identifying said random sequence or said nucleic acid sequence of interest.

194.   The method of claim 193, further comprising the step of sequencing the identified random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.

195.   The method of claim 193, further comprising performing steps 1, 2, 3 and 4 reiteratively.

196. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest, comprising:

  1. providing at least one nucleic acid molecule of claim 181;

  2. translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;

  3. contacting said at least one complex with at least one substance of interest;

  4. selecting at least one complex that binds with said at least one substance of interest; and

  5. identifying said polypeptide in said complex.

197. The method of claim 196, wherein said identifying comprises amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.

198. The method of claim 196, further comprising performing steps 1, 2, 3 and 4 reiteratively.

199. A method for identifying a test compound, comprising:

  a) contacting a target with a complex that comprises:

    1) a linking moiety;

    2) a random sequence or a sequence of interest that encodes a polypeptide; and

    3) a polypeptide encoded by said random sequence or sequence of interest;

    wherein said linking moiety is operably linked to said polypeptide;

  b) identifying polypeptides bound with said target;

  c) determining the structure of said polypeptide; and

  d) identifying moieties that have structures that have space filling shapes that are similar to at least a portion of said polypeptide.

200. A method for identifying a target, comprising:

  a) contacting a substance of interest with a complex that comprises:

    1) a linking moeity; and

    2) a random sequence or sequence of interest; and

    3) a polypeptide encoded by said random sequence or sequence of interest;

    wherein said linking moiety is operably linked to said polypeptide; and

  b) identifying targets that bind with said complex.--